

Blast 2 Sequence:

Exhibit 3

NCBI	Entrez	BLAST 2 sequences	BLAST	Example	Help
------	--------	-------------------	-------	---------	------

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site. **Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250.

Program:  Matrix: 

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch: ☐ Use MegaB/AST Strand option: Open gap:  and extension gap:  penaltiesgap x\_dropoff:  expect:  word size:  Filter: ☒Sequence 1: Enter accession or GI:  or download from file:  or sequence in FASTA format from:  to: Sequence 2: Enter accession or GI:  or download from file:  or sequence in FASTA format from:  to: 

cgaccaagtctacagcgcttcggg

 

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)  
Credits to: [Tatiana Tatusova](#) and [Tom Madden](#)

## Blast Result

 **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter: ☒ Align:

Sequence 1 gi 1307635 Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA Length 2755

Sequence 2 lcl|seq\_2 Length 25

No significant similarity was found.